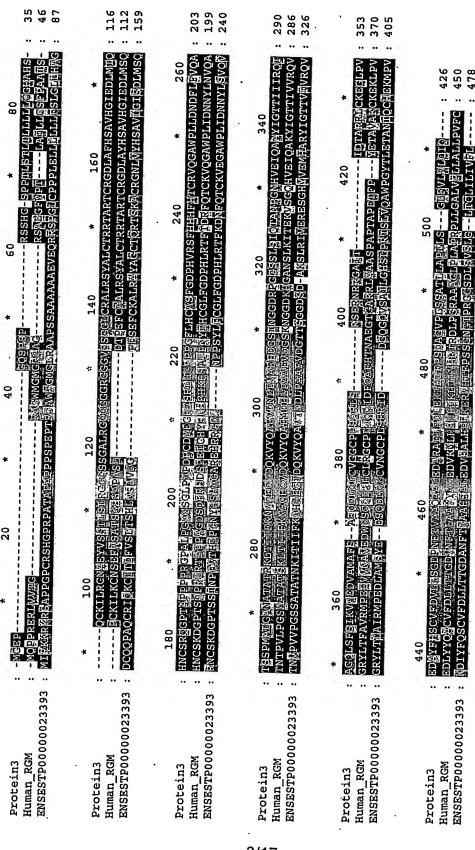


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	1	10	20	30	40	50	60	70	60	80	100	110	120	130
hunan Hus	TCTATAT	REATATION	TRRATCTRE	RERERCRES	BRECREACT	ETERTECCC	RSTCTREAT	ECTROATRO	TRESCRIGER	TRESSTATE	GATCTCTATA	TREATREAGG	THERTRERER	TATREAT
Rat Consensus	******	••••••	••••••	••••••	••••••	••••••	•••••	••••••	••••••		•••••	••••••	•••••	
	131 :	L40	150	150	170	180	190	200	210	220	230	240	250	260
hunan Hus	ATHTECC	CTATTRETT	CTGTTCCTC	TREAGRACE	CTRATECRE	GRECGTOTT	TEGRATOGE	CCTTCTGTTE	RITTCRCTTE	CRRETECTE	RRRGATERTE	RICTORGRIEN	RCCTRYGGC	TECRORS
Rat. Consensus														
CONSCISUS	261	*********	204				••••••	••••••	••••••	••••••	•••••	•••••••	••••••	•••••
	Ī		200	230	300	310	320	330	340	350	360	370	380	390
entl neand	нонтьно	116601804	100011661	TECRETATO	пеннен	TTTRRGGGG	GGTGGGGGGG	COGGGTCTCRC	TETTGCCCRS	CTGGRGTGC	RATEGCETTA	TCATRGCTCAC	TECRECCTO	RRRCTCC
Rat. Consensus	•••••	•••••	•••••	•••••	••••••	••••••	••••••	••••••	•••••	••••••	••••••	*********		•••••
•	391	100	410	420	430	440	450	460	470	480	430	500	510	520
hunan Hus	TECECTC	RETERCECT	CCTECCTC	RECTCCCRI	RETECTORG	TTTGCRITI	arrancen	RCRRGATTAT	GTTHTTCCHT	MARGTATCT	TTCTGRGGCT	RESCRICTE	TTCRCRCTT	STRATEC
Rat. Consensus	•													
00110011000	521	72A	540	EEO.	560					••••••	•••••••••••••••••••••••••••••••••••••••	• • • • • • • • • • • • • • • • • • • •	*********	•••••
hunan	COCCOCT	Teococce				5/0	580	590	600	610	620 	630	640	650
Hus Rat	CHICAL I	- i an an mac	i critari i aran	mount ILM	IGNOSCIBILI	eus i i chikiani	CURRENCT GG	CHHICATRETE	RGROCTCHTC	CEGRREGER	6GAA6GAA6G	ROGERGGGRGG	RREGEREGE	RETERRE
Consensus	•••••	•••••		•••••	********	******	••••••	••••••	•••••					
	651 (220	670	680	630	700	710	720	730	740	750	. 760	770	780
hunan	GRAGGRA	GARGGARG	ARGGRAGG	RAGGRAGGA	REGRAGGRAG	GARGGRARA	STATATTTT	GRATCTTTT	CTATTTCTCC	RCTCTTYCT	TIRGRAGART	TCTRTTTCCRT		
thus Rat									CTEGCCCCRCT					
Consensus		· · · · · · · · · · · · · · · · · · ·		••••••	•••••	********	••••••	t	ctcc	.ctct.t	.t.ga	tacca.	tcttc	.cc.ct.
	1	790	800	810	820	830	840	850	698	870	B80	890	900	910
hunan Hus		ii trecci ii	TCTCCARG	CRARTCGGG	AGCCTTTATT	TTTTGTGTAT	TTCATGRGGS TGTATT—GR	RGRGGRAGAT	GRATTGCTGTF	CARACTARA	GTRATGRARA	TGGRGTAGGTA	GERGEATRE	CRECTE
Rat Consensus	-6cc	CCCRI	CRCCCCCG	RRRCCCGGR	RECTTCTGT1 .agc.L.L.L	TTTTGTGTT LLLLgtgt.	TGTATTGE TgtATtGe	CGREGREGRE	GENTTETTEC GENTTETTEC GENTTETTEC	CRCACTRGC	GTARTGGARA	AGGTEGREATE	GRR—TRG	CRECTE
	911 9	320	930	940	950	250	970	980	990	1000	1010	1020		
hunan	CARGGATO	TGRECTEG	TREACTER	RCRARCCCT	CRTCCTARGO	RACTCRCAG	CTCRGATTYC	TTCTCTGGRC	AGCTGGCTTT				1030	1040
euff tsR	COURSETT	TERTIFICA	recerece	OTODOCCCT	CCTCCCCCCCCC	COTTCTCCT		, I I C I CLIMINE	AUGL FUBLL FE		CIEMMINGT	TGECGGRGATG	accencecto	CTCTGRR
Consensus					-	RRETCEgeti	CTCCGGTTTC	TTCTCccGAC	RECTERCETT	CGgC.TT	CTGRRATAST	Legcergate	:GGgGRGGGL	Tetera
•	1041 .10		1050	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
hunan Hus									CAGCATAGCAS CAGTARAGAGS				CRATTECCC	
Rat Consensus	ETACGCCT	GCCATC	ROTTOTAC: Catetter:	ARGCCAGCT RAGCCAGCT	ACCTC-TACE ACCTC.TACE	TACCATETE! TRCcATeTE!	TEGRARCTCA TeGRARCTCA	GTGGCATCCT	CAGTARAGAGA CAGTARAGAGA CAGTARAGAGA	GGATGAGAA	CEGTERGTER	CREGCETCRER	CRRATCACCE	1CCASCC
	1171 11		150	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	
husen	TTTTTRAC	GGCCAGGAG	CTCRACAT	TATTGRARA	TGCTGCAGGG	CTGCCTGGR	TREGCRETE	RCCRCRCRGT	CRERCRAGETO	GRATTEGAT	ATCC RECTTE	TCTCTCOTOTT	TOTOTOGY	1300
Mus Rat	STOTTBOO	REGEREGERE	CTCH	TRETERERR	CECTOORCCO	CCTCOI	T CCCCC	GT	CATACARACT	CARTTERAC	RTGGGRCTYR	GCCOTCGTTCT	ETCTTTREEC	CRGTCCC
Consensus	GIGITHO	llibelgiiha	iciuiT	THETERERA	CGCTaaRGGa	CCTG.AC	ST.GGCAG	GT	CALACARGETO	cAgTTGGAc	RTERERCTTG	¿CcaTCeTtcT	cTCTtTagg	LagTCCC
	1301 13		1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
hunan Hus	TERCTION	ICACTCRATA ITACCCAGCA	ICTCC-ATA ITTCCCATA	MCTMCT- MCCCTCTT	-AATECTOTA TATTTTGCTO	ACCETECCE! ATCATTCCT!	CTCCCCCRR CTGCCTTRE	CTCCCACACC	CTRCCCCCRCC CTRCTGCCRCC	ARCGITCCT	GGARTTTTGG	ACTTRECTATTO	TTTRABARCCC	TCARCT
Rat. Consensus	TERCTIC	TRECERBER	ITTCCCATA ILTCCcATA	TTCCCTCTT	TATTTTGCT(LALTLLeCTo	ATCRTTCCTO ALCaTLCCL	CTECCTYRE	CTCCCACACC	CTRCTGCCRCC CTRCTGCCRCC CTRCLgCCRCC	RACGITCCI	GGAATTTTGG	ACCTRGCTRTT	TTTARRACTO	TCRRCT
	1431 14		450	1460	1470	1480	1490	1500	1510	1520	1530			
hunan	COGTRGCO	RCCTCCCTC	с-стестс	AGCTGTECA	GTRCTCTGGC	CAGCCATATA						1540	1550	1560
Hus Rat	CAGGREGE	ACCTCCCTC ACCTCCCTC	CTCCTCTC CTCCTCTC	AGCTGTCCA RGCTGTCCA	GTECTTEEGC GTECTTEGGC	CARCCATATE	CTCTCCCTG	CCCCCTCCCC	CCATRCCARRO CCACRCCARRO CCACACCARRO	CTCCTCTGG	CTCTCTGRCC	CGGTGAGATT	GCRGCCAGTC	CGGGGG
Consensus	CRGgAGgC	ACCYCCETO	CtCctCTC	RGCTGTCCR	GTECTLEGGC	CRACCHTATE	CTCtccctg	CECCCTCCCC	CCACACCARRO CCACACCARRO CCACACCARRO	CTeCTCTGG	ETCLCTGRCC	Cegterent	GCRGCCaGt(Cegggg
	1561 15		.580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690
nanud Sulf	RTCGGGGG	GAGACACGE CAGACATGE	acaaccac	ATGGRGGRC	CCCCTGGCTG	GAGCTGACCE	ACAGAGTAG	GGRATCATGG	CTGGRGRATTG CTGGRGRACCG	GNTRGCAGA	GTAATGTTTG	ICCTCTGGAAA	CASTARGTCA	IARATGA
Rat Consensus	ATCGGGGA ALC _E GGG	CREACATGE CAGACALGE	RGAAGGAG RGaaggag	ATGGRGGAC atggagGAC	CCCCTGGCTG	GRECREACCE	ACAGAATAG	GCRACTATGG	CTGGRGRACCG CTGGRGRACCG CTGGRGRACCG	GGTRTCRGA	GTAATGCTTG	ICCTCGGGARA	CAGTAAGTCT	RGATGA
	1691 17		710	1720	1730	1740	1750	1760	1770					
hunan	RATTECAS	TTCCTTTRE	TARGETTT						CTCTCGTCCAR	1780	1730	1800	1810	1820
Mus Rat	RATGGCGG	TTECTTTER	TRAGCTTT	TEGETCERS	GCTAGRATTT	CATARACTTE			-::::::::::::::::::::::::::::::::::::::	нинстинын	ICILICEITA	TH-CRIRCC	CARTCY	TCRCT
Consensus	HHTGGCGG	Retriger	TRAGCITT	TeegTcGflg	GCTRGRATTT	cornangtra	CAERCA		-TCTgtTCtgN	HHHLIHHIH	ICICICA ATTRI	THEGHT RESE	CODTCT	-TCRCT
	1821 18		840	1850	1860	1870	1680	1890	1900	1910	1920	1930	1940 19	146
hunan Hus	TTCTGTCT	181116111	CTEGCETC	TGGCCTCTR	GCTTTTTGRA	GTTTERTTCT	CTGTCTCTC	CTCTGGCRGT	CTTRGCCCTCT CRGRCCCCTCC	CTTTRCCTT	TTACCTCAAC	ACTCCTGATE	RRGTTTTAGA	-1 -1
Rat Consensus	TTTGGRC-			TECTCOTOC	BUTTOTTOO	ODCDOCCCTT	TTCCCCCCCC	annuagunun	CHERCCCCTCC CREACCCCTCC CogncCCCTCc	CHITHICIL	11			
						Gungggel	riucragga	gaaaulgiiid	ragiiculli i Cc	Laa HitCTgi	:1.,EC	••••••	•••••	••

FIGURE 2



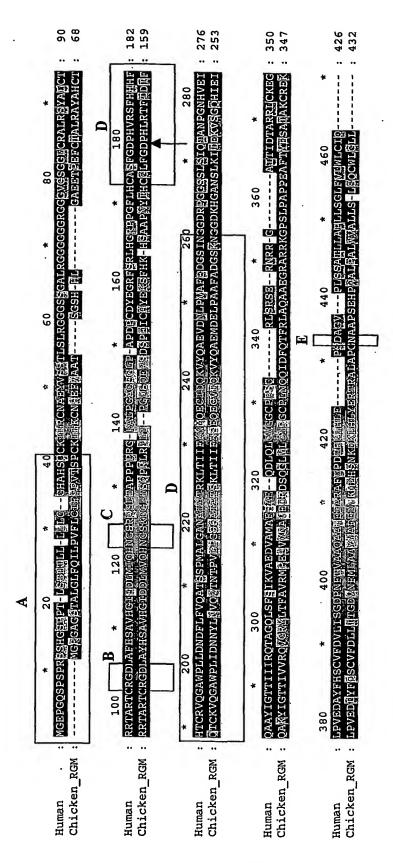


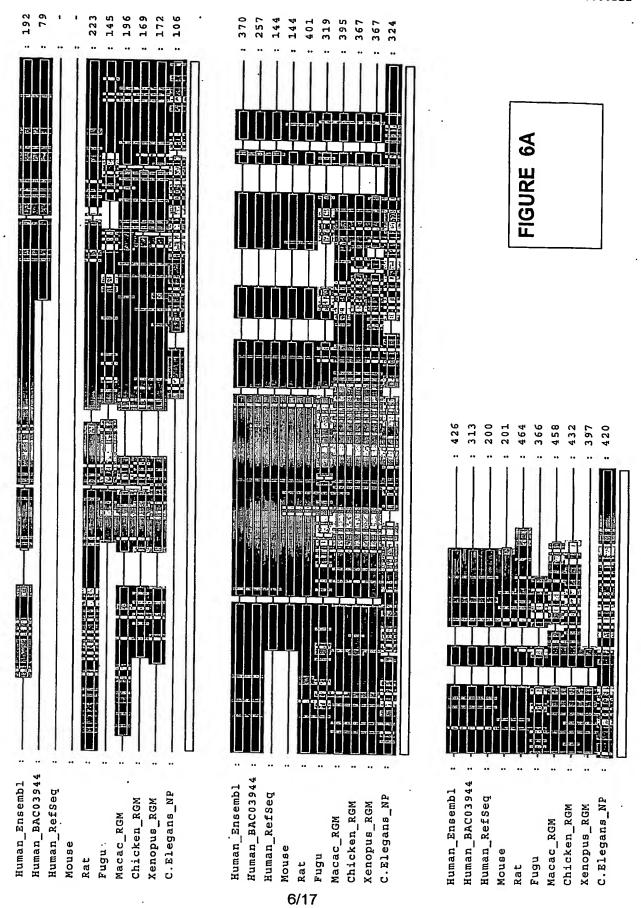
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FIGURE 4

. 0,000 0000	198 191 194 151	297 290 293 248	396 389 345	4 4 2 6 4 2 2 3 6 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
				* * * *
80 * 10 GSGGLCRALRSYALCTRRTARTCRG ASGGLCRALRSYALCTRRTARTCRG ASGGLCRALRSYALCTRRTARTCRG	160 * 180 *	260 * 280 * 280 KPGCANIGANIGANITITROTAGOLSFS REGESSLSIQTANLGSHVEIRAANIGTTIITROTAGOLSFS REGESSLSIQTANLGSHVEIRAANIGTTIITROTAGOLSFS REGESSLSIQTANLGSHVEIRAANIGTTIIVROTAGOLSFS	360 FESCVFDVØISGDPNFTVAAQBALBDARBFLBDLEMLHL FQSCVFDVSVSGDPNFTVAAQTALDDARIFLTDLENLHL FQSCVFDVSVSGDPNFTVAAQSALDDARVFLTDLENLHL BQACIFDLEMSGDENBSGAABSALBDARVFLTDLENLHL	* ! ! ! !
80 **GELCRALRSYALCTRR' 3GLCRALRSYALCTRR' 3GLCRALRSYALCTRR' 3GLCRALMSYSTICTKR'	180 RSFHEHFHTC RSFHNEFHTC RSFHNHFHTC RTFNNIPFHTC	280 SIQAAYIGTTI SIRAAYIGTTI SIRAAYIGTTI	* MISGDDNFTVAAQHALEDARE SVSGDDNFTVAAQTALDDARI SVSGDPNFTVAAQSALDDARV MISGDFNFSGAARSALGDADK	4
* #ICECVB ANAEK	* LHCASFGDPHVI THCASFGDPHVI THCASFGDPHI	60 GGSSLSIQTANEGMHVEIDAAYIGTTI GGSSLSIQTANLGSHVEIRAAYIGTTI GGSSLSIQTANLGSHVEIRAAYIGTTI GD班工AI-TDS票GAAREIRAAHI-ATV	360 YPESCVFDVØISGDPNFTV YPOSCVFDVSVSGDPNFTVY YPOSCVFDVSVSGDPNFTVY YBOACIFDLØISGDØNFTVI	* 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
60 25 Sigal Recedence 25 Sigal Recedence 25 Sigal Recedence 25 Sigal Recedence 25 Sigal Recedence 26 Sigal Recedence 27 Sigal Recedence 28 Sigal R	160 RLHGRPGFLHCASFGDPHVRSFH開HFH REHGRAPGFLHCASFGDPHVRSFHNGFH REHGRIIPGFLHCASFGDPHVRSFHNHFH REHGRIIPGFLHCENFGDPHTRTFNNIPFH	260 DRPGGSSLS1 BRPGGSSLS1 BRPGGSSLS1 BRPGGSSLS1	360 DRYFHSCVFDV DRYFOSCVFDV DRYFOSCVFDV	4
* * * * * * * * * * * * * * * * * * *	EGANATORA SANTARANGO S	* Antiboeshingee Antiboesungee Antiboesungee Antiboesungee	* ALCKORGARAND ALCKORGARAND ALCKORGARAND ALCKORGARAND ALCKORGARAND	* 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
40 Kejercnaeyv Kejercnaeyv Kejercnaeyv	140 GKGEGEPAPD GRODAPLTPD GRODAPLTPD GRODAPLTPD	240 CONTRACTORINE PROCESSENT PROC	340 Gerphidtar Gertaidtar Gertaidtar Egertaidtar Egertaidtar	44 1 1 1 1 1 1 1 1 1
* Tululicemahsog Tulifisisegahsogg Tululiceoahsoge Tululiceoahsoge	* PPPERGPALE PPPRGPAEE SPPARCEANEE	* IMOECTEDOROV IMO	* RESESERNE RESESERVE RESESERVE	*
	PTA PTA PTA	220 BRKLTILEKA TRKTTTTFFKA TRKTTTFFFKA LDKITVIKKE	320 LCVGGCPPSQ LCVGGCPPSQ LCVGGCPPSQ LCMMGCPPSQ	420 LSGLFVLWLC LSALFVLWEC LSVLFVLWEC
* MGEPGOSPSPRSSHGSPPTLSTLY MGQSPSPRSPHGSPPTLSTLY MGDRGRSPSFRSPHGSPPTLSTLY	0 DLAFHSAVHGIEDLMIQHNCSRQG DLAFHSAVHGIEDLMIQHNCSRQG DLAFHSAVHGIEDLMIQHNCSRQG DLAYHSAVQGIEDLLIQ网络C與國	220 LEVQATSSPWALGANATBERKLT. LEVQATSSPVBSGANATTTRAKTT. LEVQATSSPPRSGANATTTRKTT LYVQATSSPPRRGEØATWLDKTT	320 IKVAEDVAMAFSABODLOLGVGGG IRVAEDVARAFSABODLOLGVGGG IRVAEDVARAFSABODLOLGVGGG VKSPRSVNBAFGFBODLOLCWMGG	400 * 420 FPSDAGMPLSSATELERPLLSGLFV FPSDAGPPLSPAHCLVPLLSALFV FPMDAGPPLSPATCLVRLISMLFV ISPTSAAQREMHICLLMLES
SOBABBW:	0 DLAFHSAV DLAFHSAV DLAFHSAV DLAYHSAV	1 LFVQATSS: LFVQATSS: LFVQATSS: LYVQATSS:		
Human Mouse Rat Fugu	Human Mouse Rat Fugu	Human Mouse : Rat : Fugu .:	Human : Mouse : Rat : Fugu :	Human : Mouse : Rat : Fugu :

FIGURE 5





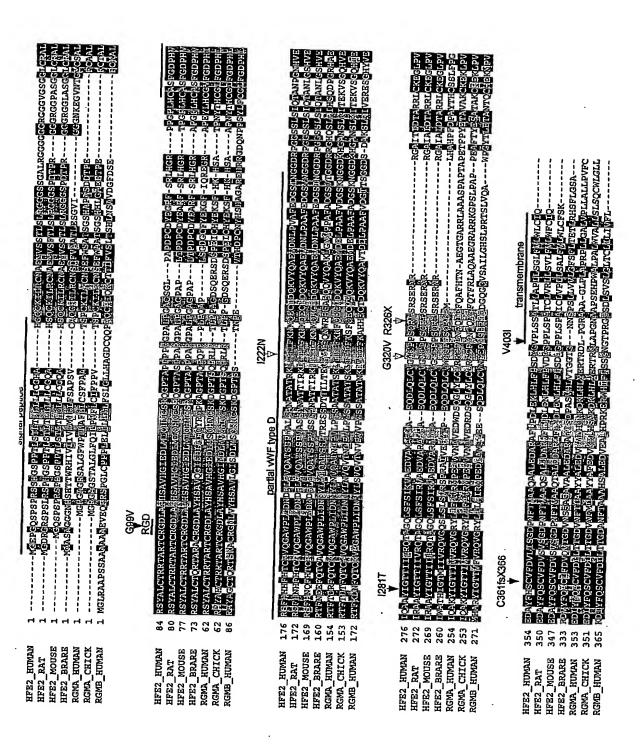
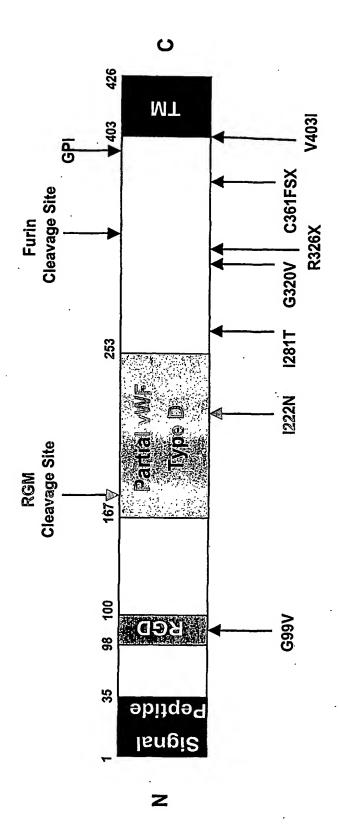


Figure 6B





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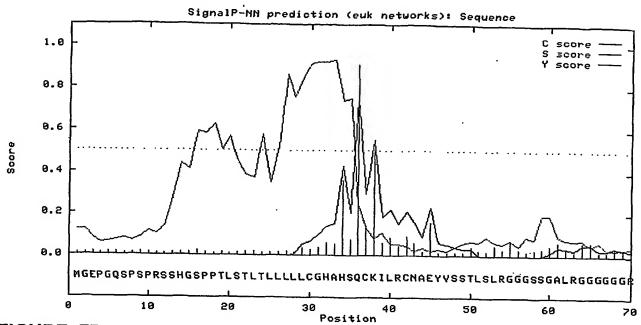


FIGURE 7B

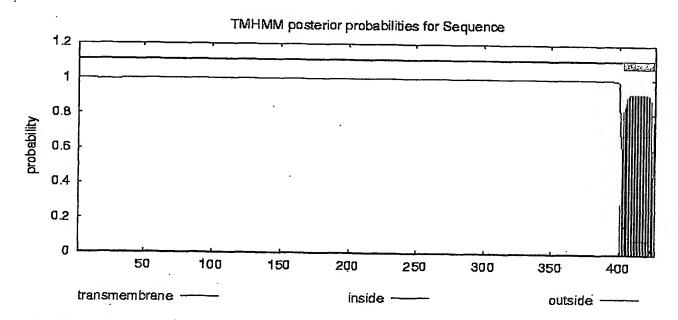


FIGURE 7C

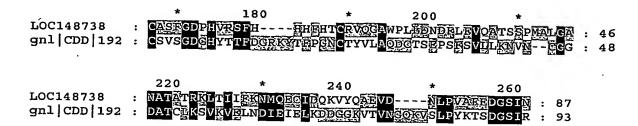


FIGURE 7D

FIGURE 7E

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FIGURE 8A

```
ATG GGGGAGCCAGGCCAGTCCCCTAGTCCCAGGTCCTCCATGGCAGTCCCCCAACTCTA
            1
           AGCACTCTCACTCTGCTGCTGCTCTGTGGACATGCTCATTCTCAATGCAAGATCCTC
 61
           -S--T--L--T--L--L--L--L--C--G--H--A--H--S--Q--C--K--I--L-
 21
           \tt CGCTGCAATGCTGAGTACGTATCGTCCACTCTGAGCCTTAGAGGTGGGGGTTCATCAGGA
 121
           -R--C--N--A--E--Y--V--S--S--T--L--S--L--R--G--G--S--S--G-
 41
           GCACTTCGAGGAGGAGGAGGAGGCCGGGGTGGAGGGGTGGGCTCTGGCGGCCTCTGT
 181
           -A--L--R--G--G--G--G--G--R--G--G--V--G--S--G--G--L--C-
 61
           CGAGCCCTCCGCTCTATGCGCTCTGCACTCGGCGCACCGCGCCCCGCACCTGCCGCGGGGAC
 241
           -R--A--L--R--S--Y--A--L--C--T--R--R--T--A--R--T--C--R--G--D-
 81
           CTCGCCTTCCATTCGGCGGTACATGGCATCGAAGACCTGATGATCCAGCACAACTGCTCC
 301
           -L--A--F--H--S--A--V--H--G--I--E--D--L--M--I--Q--H--N--C--S-
 101
           CGCCAGGGCCCTACAGCCCCTCCCCCGCCCCGGGGCCCCGCCCTTCCAGGCGCGGGCTCC
 361
 121
           -R--Q--G--P--\underline{T}--A--P--P--P--P--R--G--P--A--L--P--G--A--G--S--
           {\tt GGCCTCCCTGCCCCGGACCCTTGTGACTATGAAGGCCGGTTTTCCCGGCTGCATGGTCGT}
 421
           -G--L--P--A--P--D--P--C--D--Y--E--G--R--F--S--R--L--H--G--R-
141
           \tt CCCCCGGGGTTCTTGCATTGCGCTTCCTTCGGGGACCCCCATGTGCGCAGCTTCCACCAT
 481
           161
           {\tt CACTTTCACACATGCCGTGTCCAAGGAGCTTGGCCTCTACTGGATAATGACTTCCTCTTT}
           -H--F--H--T--C--R--V--Q--G--A--W--P--L--L--D--N--D--F--L--F-
181
           GTCCAAGCCACCAGCTCCCCATGGCGTTGGGGGCCAACGCTACCGCCACCCGGAAGCTC
601
           -V - Q - A - T - S - S - P - M - A - L - G - A - N - A - T - A - T - R - K - L - G - A - N - A - T - A - T - A - T - R - K - L - G - A - M - A - M - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T - A - T -
201
                                                                             * * *
           ACCATCATATTTAAGAACATGCAGGAATGCATTGATCAGAAGGTGTATCAGGCTGAGGTG
661
          -T--I--F--K--N--M--Q--E--C--I--D--Q--K--V--Y--Q--A--E--V-
221
721
           241
           -D--N--L--P--V--A--F--E--D--G--S--I--N--G--G--D--R--P--G--G-
          781
261
          -S--S--L--S--I--Q--\underline{T}--A--N--P--G--N--H--V--E--I--Q--A--A--Y-
841
          ATTGGCACAACTATAATCATTCGGCAGACAGCTGGGCAGCTCTCCTTCTCCATCAAGGTA
281
          -I--G--T--I--I--I--R--Q--T--A--G--Q--L--S--F--S--I--K--V-
          GCAGAGGATGTGGCCATGGCCTTCTCAGCTGAACAGGACCTGCAGCTCTGTGTTGGGGGG
901
301
          -A--E--D--V--A--M--A--F--S--A--E--Q--D--L--Q--L--C--V--G--G-
961
          TGCCCTCCAAGTCAGCGACTCTCTCGATCAGAGCGCAATCGTCGGGGAGCTATAACCATT
          -C--P--P--S--Q--R--L--S--R--S--E--R--N--R--R_AAG--A--I--T--I-
1021 GATACTGCCAGACGGCTGTGCAAGGAAGGGCTTCCAGTGGAAGATGCTTACTTCCATTCC
          -D--T--A--R--R--L--C--K--E--G--L--P--V--E--D--A--Y--F--H--S-
```

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FIGURE 8B

1081 361	TGTGTCTTTGATGTTTTAATTTCTGGTGATCCCAACTTTACCGTGGCAGCTCAGGCAGCACACACA
	◆ ♦ ◆
1141	CTGGAGGATGCCCGAGCCTTCCTGCCAGACTTAGAGAAGCTGCATCTCTTCCCCTCAGAT
381	-LEDARAFLPDLEKLHLFPSD-
1201	GCTGGGGTTCCTCTTTCCTCAGCAACCCTCTTAGCTCCACTCCTTTCTGGGCTCTTTGTT
101	-AGVPLSSATLLAPLLSGLFV-
1261 121	CTGTGGCTTTGCATTCAGTAAGGGGACCATCAGTCCCATTACTAGTTTGGAAATGATTTG
I & -L	

FIGURE 9

Open circle/square = Unknown (no data)

Crossed circle/square = Unaffected

Filled circle/square = Affected

Grey circle/square = Unknown (ambiguous)

Slash circle/square = Deceased

OP'H7

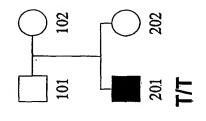


FIGURE 9A

